

SEQUENCE LISTING

<110> BOUGUELERET; Lydie  
CUSIN; Isabelle

<120> SECRETED POLYPEPTIDE SPECIES ASSOCIATED  
WITH CARDIOVASCULAR DISORDERS

<130> DV/4-33628A/GEP US-P

<140> 10/561,292  
<141> 2005-12-20

<150> 60/484,153  
<151> 2003-06-30

<150> PCT/EP2004/007047  
<151> 2004-06-29

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 456  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PROPEP  
<222> (1)...(456)  
<223> Precursor protein of CP22

<400> 1  
Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly  
1 .  
Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu  
20 .  
Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr  
35 .  
Gly Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys  
50 .  
Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His  
65 .  
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys  
85 .  
Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys  
100 .  
Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro  
115 .  
Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro  
130 .  
Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro  
145 .  
Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Glu Gln

165	170	175
Gln	Glu	His
Leu	Leu	Gly
Asp	Leu	Gln
180	185	190
Asp	Ser	Leu
Pro	Gly	Leu
Trp	Lys	Ala
195	200	205
Ala	Ser	Leu
Ser	Asn	Asp
Val	Lys	Asn
210	215	220
Glu	Ala	Gly
Ala	Gly	Ala
225	230	235
His	Asn	Ala
Leu	Phe	Ala
Thr	Gln	Arg
245	250	255
Leu	Phe	His
Ser	Leu	Phe
Gly	Asn	Gly
260	265	270
Val	Ser	Leu
Asp	Gly	Lys
275	280	285
Lys	Lys	Gln
290	295	300
Glu	Ala	Glu
305	310	315
Ala	Leu	Gly
Ala	Ala	Leu
Trp	Glu	Ala
325	330	335
Ala	Ser	Phe
Ser	Glu	Gly
340	345	350
Thr	Thr	Tyr
Ile	Asn	Ile
Gly	Ser	Ser
355	360	365
Phe	Arg	Ala
Pro	Glu	Arg
370	375	380
Phe	Gly	Pro
385	390	395
Arg	Thr	Pro
Val	Cys	Thr
Thr	Gly	Gln
405	410	415
Val	Phe	Ala
Met	Ala	Glu
Leu	Gln	Lys
420	425	430
Leu	Thr	Gln
Gly	Ser	Ile
435	440	445
Gly	Gly	Phe
450	455	

<210> 2  
<211> 433  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)...(433)  
<223> Polypeptide sequence of SEQ ID NO:1 after removal  
of the signal peptide

<400> 2  
Ala Ser Ser Thr Ser Leu Ser Asp Leu Gln Ser Ser Arg Thr Pro Gly  
1 5 10 15  
Val Trp Lys Ala Glu Ala Glu Asp Thr Ser Lys Asp Pro Val Gly Arg  
20 25 30  
Asn Trp Cys Pro Tyr Pro Met Ser Lys Leu Val Thr Leu Leu Ala Leu  
35 40 45

Cys Lys Thr Glu Lys Phe Leu Ile His Ser Gln Gln Pro Cys Pro Gln  
   50               55               60  
 Gly Ala Pro Asp Cys Gln Lys Val Lys Val Met Tyr Arg Met Ala His  
   65               70               75               80  
 Lys Pro Val Tyr Gln Val Lys Gln Lys Val Leu Thr Ser Leu Ala Trp  
   85               90               95  
 Arg Cys Cys Pro Gly Tyr Thr Gly Pro Asn Cys Glu His His Asp Ser  
  100               105              110  
 Met Ala Ile Pro Glu Pro Ala Asp Pro Gly Asp Ser His Gln Glu Pro  
  115               120              125  
 Gln Asp Gly Pro Val Ser Phe Lys Pro Gly His Leu Ala Ala Val Ile  
  130               135              140  
 Asn Glu Val Glu Val Gln Gln Glu Gln Gln Glu His Leu Leu Gly Asp  
  145               150              155              160  
 Leu Gln Asn Asp Val His Arg Val Ala Asp Ser Leu Pro Gly Leu Trp  
  165               170              175  
 Lys Ala Leu Pro Gly Asn Leu Thr Ala Ala Ser Leu Ser Asn Asp Val  
  180               185              190  
 Lys Asn Val Gly Arg Cys Cys Glu Ala Glu Ala Gly Ala Ala Ala  
  195               200              205  
 Ser Leu Asn Ala Ser Leu His Gly Leu His Asn Ala Leu Phe Ala Thr  
  210               215              220  
 Gln Arg Ser Leu Glu Gln His Gln Arg Leu Phe His Ser Leu Phe Gly  
  225               230              235              240  
 Asn Phe Gln Gly Leu Met Glu Ala Asn Val Ser Leu Asp Leu Gly Lys  
  245               250              255  
 Leu Gln Thr Met Leu Ser Arg Lys Gly Lys Lys Gln Gln Lys Asp Leu  
  260               265              270  
 Glu Ala Pro Arg Lys Arg Asp Lys Lys Glu Ala Glu Pro Leu Val Asp  
  275               280              285  
 Ile Arg Val Thr Gly Pro Val Pro Gly Ala Leu Gly Ala Ala Leu Trp  
  290               295              300  
 Glu Ala Gly Ser Pro Val Ala Phe Tyr Ala Ser Phe Ser Glu Gly Thr  
  305               310              315              320  
 Ala Ala Leu Gln Thr Val Lys Phe Asn Thr Thr Tyr Ile Asn Ile Gly  
  325               330              335  
 Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Glu Arg Gly  
  340               345              350  
 Val Tyr Leu Phe Ala Val Ser Val Glu Phe Gly Pro Gly Pro Gly Thr  
  355               360              365  
 Gly Gln Leu Val Phe Gly Gly His His Arg Thr Pro Val Cys Thr Thr  
  370               375              380  
 Gly Gln Gly Ser Gly Ser Thr Ala Thr Val Phe Ala Met Ala Glu Leu  
  385               390              395              400  
 Gln Lys Gly Glu Arg Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr  
  405               410              415  
 Lys Arg Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys  
  420               425              430  
 Thr

<210> 3  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)...(152)  
<223> Cardiovascular disorder Plasma Polypeptide 22 (CPP  
22)

<400> 3  
Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly  
1 5 10 15  
Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr  
20 25 30  
Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn  
35 40 45  
Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr  
50 55 60  
Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu  
65 70 75 80  
Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His  
85 90 95  
Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr  
100 105 110  
Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu  
115 120 125  
Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe  
130 135 140  
Gly Gly Phe Leu Met Phe Lys Thr  
145 150

<210> 4  
<211> 24  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)...(24)  
<223> Tryptic peptides of CPP 22 found by MS-MS mass  
spectrometry in plasma samples of individuals with  
coronary artery disease

<400> 4  
Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr Val  
1 5 10 15  
Phe Ala Met Ala Glu Leu Gln Lys  
20

<210> 5  
<211> 12  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)...(12)  
<223> Tryptic peptides of CPP 22 found by MS-MS mass

spectrometry in plasma samples of individuals with  
coronary artery disease

<400> 5  
Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr Lys  
1 5 10

<210> 6  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)...(14)  
<223> Tryptic peptides of CPP 22 found by MS-MS mass  
spectrometry in plasma samples of individuals with  
coronary artery disease

<400> 6  
Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys  
1 5 10

<210> 7  
<211> 1371  
<212> DNA  
<213> Homo sapiens

<220>  
<221> variation  
<222> (1)...(1371)  
<223> Splice variant of the Endoglyx-1 gene and  
comprises the cDNA coding sequence for SEQ ID NO:  
1

<400> 7  
atgatcctga gtttgctgtt cagcctggg ggccccctgg gctgggggct gctggggca 60  
tggggccagg cttccagtac tagcctctct gatctgcaga gctccaggac acctggggtc 120  
tggaggcag aggctgagga caccggcaag gacccctgtag gacgtaactg gtgcccctac 180  
ccaatgtcca agctggtcac cttactagct ctttgcaaaa cagagaaaatt cctcatccac 240  
tcgcagcagc cgtgtccgca gggagctcca gactgccaga aagtcaaagt catgtaccgc 300  
atggcccaca agccagtgtt ccaggtcaag cagaagggtgc tgacctcttt ggcctggagg 360  
tgctgcctg gctacacggg ccccaactgc gaggcaccacg attccatggc aatccctgag 420  
cctcgagatc ctggtgacag ccaccaggaa cctcaggatg gaccagtcaag cttcaaaacct 480  
ggccaccttg ctgcagtgat caatgggtt gaggtgcaac aggaacacgca ggaacatctg 540  
ctggagatc tccagaatga tttgcaccgg gtggcagaca gcctgccagg cctgtggaaa 600  
gcctgcctg gtaacctcac agtgcacagg ctgagcaacg acgtcaagaa tgtcgggg 660  
tgctgcgagg ccgaggccgg gggcgccggc gcctccctca acgcctccct tcacggccctc 720  
cacaacgcac tcttcggcac tcagcgcagc ttggagcagc accagcggt cttccacagc 780  
ctcttggga acttccaagg gtcatacgaa gccaacgtca gcctggact gggaaagctg 840  
cagaccatgc tgagcaggaa aggaagaag cagcagaaag acctggaagc tccccggaaag 900  
agggacaaga aggaagcgga gccttgggt gacatacggtt tcacaggccc tgtgccagg 960  
gccttggcg cgccgctctg ggaggcagga tccctgtgg ccttctatgc cagctttca 1020  
gaagggacgg ctgcccgtca gacagtgaag ttcaacacca catacatcaa cattggcagc 1080  
agctacttcc ctgaacatgg ctacttccga gcccctgagc gtggtgtcta cctgtttgca 1140

gtgagcgttg aatttggccc agggccaggc accgggcagc tggtgttgg aggtcaccat 1200  
cgactccag tctgtaccac tggcagggg agtggaaagca cagcaacggt ctggccatg 1260  
gctgagctgc agaagggtga gcgagtatgg tttgagttaa cccagggatc aataacaaag 1320  
agaagcctgt cgccactgc atttggggc ttccctgatgt ttaagacctg a 1371

<210> 8  
<211> 417  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)...(417)  
<223> Q8K1Z7, a murine homologue of SEQ ID NO:1

<400> 8  
Met Ile Pro Thr Leu Leu Gly Phe Gly Val Tyr Leu Ser Trp Gly  
1 5 10 15  
Leu Leu Gly Ser Trp Ala Gln Asp Pro Gly Thr Lys Phe Ser His Leu  
20 25 30  
Asn Arg Pro Gly Met Pro Glu Gly Trp Arg Leu Gly Ala Glu Asp Thr  
35 40 45  
Ser Arg Asp Pro Ile Arg Arg Asn Trp Cys Pro Tyr Gln Lys Ser Arg  
50 55 60  
Leu Val Thr Phe Val Ala Ala Cys Lys Thr Glu Lys Phe Leu Val His  
65 70 75 80  
Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Gly Val Arg  
85 90 95  
Val Met Tyr Arg Val Ala Gln Lys Pro Val Tyr Gln Val Gln Gln Lys  
100 105 110  
Val Leu Ile Ser Val Asp Trp Arg Cys Cys Pro Gly Phe Gln Gly Pro  
115 120 125  
Asp Cys Gln Asp His Asn Pro Thr Ala Asn Pro Glu Pro Thr Glu Pro  
130 135 140  
Ser Gly Lys Leu Gln Glu Thr Trp Asp Ser Met Asp Gly Phe Glu Leu  
145 150 155 160  
Gly His Pro Val Pro Glu Phe Asn Glu Ile Lys Val Pro Gln Glu Gln  
165 170 175  
Gln Glu Ile Arg Arg Leu Ser Ser Asp Val Lys Gln Ile Gly Gln Cys  
180 185 190  
Cys Glu Ala Ser Trp Ala Ala Ser Leu Asn Ser Ser Leu Glu Asp Leu  
195 200 205  
His Ser Met Leu Leu Asp Thr Gln His Gly Leu Arg Gln His Arg Gln  
210 215 220  
Leu Phe His Asn Leu Phe Gln Asn Phe Gln Gly Leu Val Ala Ser Asn  
225 230 235 240  
Ile Ser Leu Asp Leu Gly Lys Leu Gln Ala Met Leu Ser Lys Lys Asp  
245 250 255  
Lys Lys Gln Pro Arg Gly Pro Gly Glu Ser Arg Lys Arg Asp Lys Lys  
260 265 270  
Gln Val Val Met Ser Thr Asp Ala His Ala Lys Gly Leu Glu Leu Trp  
275 280 285  
Glu Thr Gly Ser Pro Val Ala Phe Tyr Ala Gly Ser Ser Glu Gly Ala  
290 295 300  
Thr Ala Leu Gln Met Val Lys Phe Asn Thr Thr Ser Ile Asn Val Gly  
305 310 315 320  
Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Lys Arg Gly

